

Run on: November 29, 2001, 08:52:45 ; Search time 10554.9 Seconds

10137.587 Million cell updates/sec

Title: US-09-526-329-40
Perfoot count: 6496

Sequence: 1 tcctcctcctccccctctc.....gttcattcagcagcagac 6486

Scoring table: IDENTITY_NUC

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 08

Listing first 45 summaries

Database :

1:	gem1	gb_ba:	*
2:	gb_hlg:	*	
3:	gb_in:	*	
4:	gb_om:	*	
5:	gb_ov:	*	
6:	gb_pat:	*	
7:	gb_ph:	*	
8:	gb_pl:	*	
9:	gb:	*	
10:	gb_ro:	*	
11:	gb_sts:	*	
12:	gb_sy:	*	
13:	gb_un:	*	
14:	gb_vl:	*	
15:	em_ba:	*	
16:	em_fun:	*	
17:	em_hum:	*	
18:	em_in:	*	
19:	em_om:	*	
20:	em_ov:	*	
21:	em_pac:	*	
22:	em_ph:	*	
23:	em_pl:	*	
24:	em_ro:	*	
25:	em_sts:	*	
26:	em_sy:	*	
27:	em_un:	*	
28:	em_vl:	*	
29:	em_hlg:	hum:	*
30:	em_hlg:	inv:	*
31:	em_hlg:	rod:	*
32:	em_hlg:	hum:	*
33:	em_hlg:	inv:	*
34:	em_hlg:	rod:	*
35:	em_hlg:	other:	*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
C 1	6485	100.0	6486	9			AL110465	Homo sapi
C 2	6443.8	99.3	166308	9			CNS010D2	AL139020 Human chr10
C 3	6369.4	98.5	210791	9			CBS021D7	AL133467 Human chr1
C 4	1633.4	25.2	1717	9			AB025274	Homo sapi
C 5	1338.5	20.6	1722	9			AB018553	Homo sapi
C 6	701.2	10.8	1152	9			AL110466	Homo sapi
C 7	701.2	10.8	3144	9			AB035343	Homo sapi
C 8	701.2	10.8	3240	9			AB035342	Homo sapi
C 9	701.2	10.8	3532	9			AB035340	Homo sapi
C 10	701.2	10.8	3539	9			AB035341	Homo sapi
C 11	699.8	10.8	1177	9			AL137027	Homo sapi
C 12	644.4	9.9	763	9			AB025272	Homo sapi
C 13	570.4	8.8	110879	9			AB025272S2	Homo sapi
C 14	506	7.8	110879	9			AC016603	Homo sapi
C 15	506	7.8	114438	9			AC010356	Homo sapi
C 16	506	7.8	204843	9			AC010359	Homo sapi
C 17	497.6	7.7	1248	9			AP111047	Homo sapi
C 18	493.8	7.6	137808	9			AC008889	Homo sapi
C 19	490	7.6	15515	9			AL133467	Homo sapi
C 20	478.6	7.4	174095	9			AL1360718	Homo sapi
C 21	474.8	7.3	172757	9			AL136788	Homo sapi
C 22	472	7.3	173185	9			AC009127	Homo sapi
C 23	467.4	7.2	186497	9			AL1031476	Homo sapi
C 24	467.2	7.2	192876	9			AC003551	Homo sapi
C 25	466.4	7.2	145442	9			AC004859	Homo sapi
C 26	466	7.2	120766	9			AC004150	Homo sapi
C 27	463	7.1	124400	9			AC008758	Homo sapi
C 28	462.6	7.1	100732	9			AL133467	Homo sapi
C 29	462.2	7.1	150036	9			AP000557	Homo sapi
C 30	462	7.1	169997	9			AC008440	Homo sapi
C 31	460.8	7.1	206836	9			AC011501	Homo sapi
C 32	459	7.1	171523	9			AC021616	Homo sapi
C 33	457.2	7.0	211543	9			AC025165	Homo sapi
C 34	456	7.0	145631	9			AC0095116	Homo sapi
C 35	454.8	7.0	169237	9			AC0090516	Homo sapi
C 36	454.8	7.0	176051	9			AC023480	Homo sapi
C 37	454.6	7.0	121266	9			AC007957	Homo sapi
C 38	454.4	7.0	149618	9			AP000556	Homo sapi
C 39	454.4	7.0	157086	9			AP000552	Homo sapi
C 40	450.2	6.9	179260	9			AC084291	Homo sapi
C 41	448.6	6.9	212656	9			AC007957	Homo sapi
C 42	446.6	6.9	199287	9			AC023157	Homo sapi
C 43	444.6	6.9	157756	9			AC007003	Homo sapi
C 44	444	6.8	97078	9			AC005841	Homo sapi
C 45	443.6	6.8	172800	9			AL1336597	Homo sapi

ALIGNMENTS

RESULT	1			
LOCUS	AF110465			
DEFINITION	AF110465	6486 bp	DNA	PRI
ACCESSION	AF110465			18-MAR-1999
VERSION	AF110465.1			
KEYWORDS	GT4324702			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Ekumoyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 6486)			
AUTHORS	Pekarsky,Y., Hallas,C., Isobe,M., Russo,G. and Croce,C.M.			
TITLE	Abnormalities at 14q32.1 in T cell malignancies involve two oncogenes			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	96 (6),	2949-2951	(1999)
MEDLINE	99178995			
REFERENCE	2 (bases 1 to 6486)			
AUTHORS	Pekarsky,Y., Hallas,C. and Croce,C.M.			

QY 1741 gcggctgaggtcactgggtgtagtggctcactgcacccacccacagctcaag- 1800
 |||||
 Db 1741 GCGGCTGAGGTGACTGGTGTGATGTTGGCTCAGTCGACCTCCACCTCCAGGCTCAAG- 1800
 QY 1801 tgattctcagtcacagccctcccgagtagcttgattcaagcgattcttttcaagtt- 1860
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 Db 1801 TGATTCTCAAGGCTCAGGCTCCGAGTAGCTTGATTCAGGCGATTGTTTTTTCACGTT- 1860
 QY 1861 aattttttgtattctcagagagacaaagttaaactgtaggccaagcttgattt- 1920
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 Db 1861 AATTTTTTGTATTCTCAGAGAGACAAAAGTTTATATGAGGCGCAGGCTGTTTT- 1920
 QY 1921 gaactcctgactcaagtgatctgcgcaacttgccctcccaagtgctgggattacagt- 1980
 |||||
 Db 1921 GAATCTCTGACCTCAAGTAGATCTGCCACCTTGCCCTCCCAAAATGCTGGGATTCAGGT- 1980
 QY 1981 gagccaactgcgcagcagttcacttgacacttaaacatataacacattccctaa- 2040
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 Db 1981 GAGCCACTCGGCCAGCCAGTTCACTGACCTTTAAACAATATATACATTTCTTAATAA- 2040
 QY 2041 aagttcaaataggtattctcaaaaaagtgttgtaagagacatgaaagcctttctgac- 2100
 |||||
 Db 2041 AAGTTCAAAATAGGTATTTCAAAAAATGTTGGTAGAAGACATGGAAGGCTTTCTGTAC- 2100
 QY 2101 atacactaaataagcagcagcaaaatltgtgagcaaatlttlaagttttlcaaaagct- 2160
 |||||
 Db 2101 ATACACTAAATTAAGCATGCAAAAATTTGTGAGCAAAATATTTTAACTTTTCAAAAGCTT- 2160
 QY 2161 gaaaagtgttaatgtagggcgacgtgtaaaatgtgtgcacccacttggaaaaaagaattag- 2220
 |||||
 Db 2161 GAAAAAGTGTAAATGAGAGGCACTGTAAATGTGTGAGCACTATGGAATAACAGGATAG- 2220
 QY 2221 gatttctcaaaaaaagaattacggtcatabatccagcaatgacacttctgatalatacca- 2280
 |||||
 Db 2221 GATTTCCTCAAAAAAAGAAATTAACGGCATTAATCCAGCAATATGCACTTCTGGATTATACCCA- 2280
 QY 2281 caagactctgaagccggaacttaagcagtattcatatcatcagtttccacagcattaca- 2340
 |||||
 Db 2281 CAAGACTCTGAAGCCGGAACCTTAAGCATGTATTCATCATCTGTTCAACAGCATATACA- 2340
 QY 2341 ttcatctagtcacaaagtgtgtgagagcccggtgtccattgatatagtaatgagtaaac- 2400
 |||||
 Db 2341 TTCTACTTACCCAAAAGGTGTGTCACCCCGCTGTCTATGTAGATGATGAGGTAAAC- 2400
 QY 2401 aacacaacatgaagatltacacccctaaagtcagacacacagcagatgaacttgagaca- 2460
 |||||
 Db 2401 AACACAACCATGAAGTATTCACCCCTTAATAAGTCAGACACACAGGATGAACCTTGGAGCCA- 2460
 QY 2461 ttatactaaatgaataatgacagtcacggaagacagattctctgtatgaggtactag- 2520
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 Db 2461 TTATACTAAATGAATATATGCCAGTCAGGAAGACAGATCTCTTGTATAGGTACTAG- 2520
 QY 2521 agtgcgtcattcatlaaagtgaatgtgtaagtcgagggcttggaaggaatcgagagatgtg- 2580
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 Db 2521 AGTGCCTCATTCATTAAGTGAATGTGACTGCCAGGGGCTGAGGAGATGCAAGGATGG- 2580
 QY 2581 gaagttaagttaagtaacaggtacgaggtctcaggttttgggaagataaaagttctggag- 2640
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 Db 2581 GAAGTTAATGTATGTAACAGGTACGAGGAGTCTCACTTTGGGAAGATTAATAAGTTCTGGAGG- 2640
 QY 2641 ttgagatgtcgagcaggtttccacatgltcaatgacattatgcccacaaacagctgacttaa- 2700
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 Db 2641 TTGAGATGCGCGAGGCTTCACATGATCAATGCACTTAATGACACCAAACTGTACTCTTAA- 2700
 QY 2701 aaaaagttgaagcgggagcaggtgtgctcaagcgttaaatcccaacatttgggagagcgaag- 2760
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 Db 2701 AAACAGTTGACCGGGCAGCGTGGCTCAAGCTTAATCCAGACTTTGGGGGACGAGGCG- 2760
 QY 2761 gggcgagatcaaaagtcagagagatcgagacatcctggtctaaacaggttgaaacccgctct- 2820
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 Db 2761 GGGCGGATCAACAAGTCAAGAGATCGAGACATCTGCGTAAACAGGTGAAACCCCGTCT- 2820
 QY 2821 ctactaaaaatacaaaagaattagccgggtgctgagggcgctgtagttccacagctac- 2880

Db 2821 CTACTAAATATCAAAAGAAATATAGCCGGGTGGGTTGGGGGCTGTGTATGCCACGCTAC- 2880
 QY 2881 tcgggggagctgtaggagagagaaatgcttgaaccttggagagcggaagcttgcgtgtagctga- 2940
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 Db 2881 TCGGGGGGCTGAGGAGGAGAAATGGCTTTAACTGTGGAGCGGAGGCTTGCAGTAGCTGGA- 2940
 QY 2941 gatccagcacttgacactccagccttgggcagacagagacactcgtctcaacaacaa- 3000
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 Db 2941 GATCCAGCCCACTGCACTGCACGCTGGGCGACAGACCAAGACTCCGTCTCAAAACAAACAA- 3000
 QY 3001 agaaaaaacaacaggttaagatttttttttttaatgattcagtaggaaataga- 3060
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 Db 3001 AGCAAAACAAAATAACAGTAAATTTTTTTTTTTTTTAAATGATTCAGTGGAAATAGA- 3060
 QY 3061 atgagatcttcaataacttagccagcgggtggagtaaggaagcacttagtaagatttt- 3120
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 Db 3061 ATGGAATCTTCAAAATAACTTATAGCCAGGGTGGGATTAAGGCACTTATGTAAGTATTTT- 3120
 QY 3121 ttccctcttcttcttaaaaaataagatcagatgtcttaggttggagattagccttctggg- 3180
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 Db 3121 TTCCCTCTTCTTTCTTAATAATATAGATGATCTTTAGGTGGGAATTAAGCTTCTCGGGCG- 3180
 QY 3181 acacatctaatgcaaaagatcagccacttctctgtaaaagatctgtagtaaacattt- 3240
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 Db 3181 ACACATCTAATGCAAAAGATCAGCCACCTTTTCTGTAAAGATCTGATGTAAACATTTT- 3240
 QY 3241 ccacttgaagcctatgctcttgcagcactcagctgctgtattgagcagtaaaagagct- 3300
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 Db 3241 CCACCTTGAAGCTATGCTCTTGTGACGACTACGCTGTGCTATTTGCAAGTCAAAACAGCT- 3300
 QY 3301 aaagcgaacggttaaaaggaaatgacggaagagccttagttattatcaataaagcttatt- 3360
 |||||
 Db 3301 AAAGCGAACGCTTAAAGGAATGACGAGGAGGCTTATTTTAACTTAATAAAGCTTTATTT- 3360
 QY 3361 tgcaaaagcagatgcaagccagacattagttctgtagatctgtatctcaacagtcgaataga- 3420
 |||||
 Db 3361 TGCAAAAGCAGATGACAGCCAGACTTAGTTGCTGTGATCTGTGATTCAGTCAGTAATACA- 3420
 QY 3421 cagagaaaggagagatttgcgcgtataatttaaatattctctcttgcgaagcagctcat- 3480
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 Db 3421 CAGAGAAAGGAGATTTTGGCGTAAATTTAAATATCTCTTTTGCATAAAGCAAGTCCAT- 3480
 QY 3481 aaaaaaagttaggaacaacaacttgaagaaattatccaacatgctgtatgtatagac- 3540
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 Db 3481 AAAAAAGTAGGACACAAACTGAGAAAAATTTATTCAAACATGCTGATGTAGTAGGC- 3540
 QY 3541 actatattcttaattcaaaaagaacatttatcaaaaagaagaacaaactatgaaat- 3600
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 Db 3541 ACTAATATCTTAAATTCAAAAGACATTTTATACAAAAGACAAATATCTTAATAAT- 3600
 QY 3601 ttgtcaaaagacttccatatttgttgcataacgttagaagccttggtttacttctcta- 3660
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 Db 3601 TGTCAAAAGACTTTCATTTTGTGTCATTAAGCTGAGGAAGCTTGTGTTACTTTCCTTA- 3660
 QY 3661 tcaatcttcaactccagtcacagcactaatttgaattttatattatattatatt- 3720
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 Db 3661 TCATCTTTCACTTCCAGTACAGCTTAATTTTGTATTTTATTTATTTATTTATTTATTT- 3720
 QY 3721 ttgagacagagcttgcgtctctccagcgtgagatgacgtgacgtacgtacgtac- 3780
 |||||
 Db 3721 TTGAGAGAGAGTCTGTGCTGTCTCCAGGCTGGAGTGCATGTGCGAGTACCTTAC- 3780
 QY 3781 aacagccttactcctccaggttcaagaaatccttccacacttagcttcccgatagctgg- 3840
 |||||
 Db 3781 AAACGCTCTACTCTCCAGGTTCAAGAAATCTTTCACCTTAGCTTCCGATTAAGCTGG- 3840
 QY 3841 acgttagacatgcccacatgcccagtaattttatcttctgttagagacagagctc- 3900
 |||||
 Db 3841 ACTGTAGGCAATGCGACCATGCGCACTTAATTTTATTTTATTTTATTTTATTTTATTTT- 3900
 QY 3901 attatgttcggagctgtgtcttgaactgtgcttcaagcagcctcctgctgagcct- 3960
 |||||

D	3901	ATATGTTGCCGAGCGCTGGCTTCAACATCGTGGCTTCAAGACAGTCCCTCGCTTGGCTC	3960
O	3961	cccaaaagtgttggatttaagaagcaaaagcaactgctcccaagctcttatccatattac	4020
D	3961	CCCAAAAGTGTGGGATTTACAGCATTAAGCCACTGCTCCCAAGCTTTATTCGATATTTAC	4020
O	4021	tataagtgttgaagtcgatgcagaactgcacataatttggcgggaaatcatcac	4080
D	4021	TATAAGTGTGGAAGGTCTATGATCAGAACAGCCATATTTTGGCCGGAATAATCTATCAC	4080
O	4081	ccctcagatcccaagagacgcgatcatctgttctttaaacaagatttaaaaattacag	4140
D	4081	CCCTCAGATCCAGGAGTCCATGGATATCTTGTTTAAACGAGATTTMAAAATTACGG	4140
O	4141	caatggcggagatggggggcccaagaagaataaccagctttaaccaagtgltgacagtt	4200
D	4141	CAATGGCGGAGATGGAGGCCCAAGAAATTCACACTTTAAACCAAGGTGTTGACAGTT	4200
O	4201	ggaaaacagtgtgctaaatttttgggatttgcagtggggcaggcaggtgtcaggtcagaaggt	4260
D	4201	GGAAACAGTGTGCTTAATTTTGGGATTTGCAGTGGGGCCAGGCAAGGTGCAGAGTGG	4260
O	4261	gccaaagaaggccccaagccatccctgatgtgagacacaagatccagtgccaaagctctgtt	4320
D	4261	GCCAAAGAGGCCCCAGCCACTCCCTGATGTGAGCACAAGTACAGTGTCCCAAGCTCTGGT	4320
O	4321	ctggagattctgaaaaatttatctctcgaccctggcagcccaatggtcatgtgtgtgc	4380
D	4321	CTGGAGATTCTGAAAATTTATACCTCTGACCCGAGACCCACATGGCAATTCCTGTGTGC	4380
O	4381	agcccaagttgcaggagaaacctatcaatgatattggcgcctctttcttgltcccttaagta	4440
D	4381	AGCCCAAGTTGGCAGGAGAACCTTATCATCATATTGGCCCTCTTCTTGTGCCCTCAGTA	4440
O	4441	tgaaccaagatcaacaagtgcaactgttggcagaatggcagtgcaataccggagagctacttc	4500
D	4441	TGAACCAAGATCAACAGTGCACCTGTGGCAGATGGCAGTGCATACCCGAGACTACTTC	4500
O	4501	ctccggcccaatgtccctcttccagctgtccgcgcgtgttggcagctctaccccgaggagaa	4560
D	4501	CTCCGGCCCAATGTCCTCTTCCAGCTGTCCAGCTGCCGCCGTGTGGCACTTACCCCGGAGAA	4560
O	4561	gtaccagacagcggatctcaattctcctgggaaatagcagaaccaatggccagcaagtgtgt	4620
D	4561	GTAACGACAGCGCCGATTCCAATTTCTGGGAATAGCAGAACATGGCCAGCAAGTGTGC	4620
O	4621	gtggtctcaaggtaaagaagaaaggtggccctggatgcacgttggccctctctctctg	4680
D	4621	GTGGTCTCAAGTAAAGGAGGAGGTGGCCCTGGATGCACTGCCGTGCTCTCTCTTCTG	4680
O	4681	tggccctggccctcttgggtgtctgtctgtccctctctctgtgtcctaagtcttcccta	4740
D	4681	TGCCCTTGCCCTCTGGGGTCTTCTGTCTGTCTTCTTCTCTGTGTCTAAAGTCTCTCTTCA	4740
O	4741	aggaagaccttgagtggtgttgggttgatctcgtgtgcaatgatttccacgttggagtgcaagcag	4800
D	4741	AGGAGACCTTGAGTGTGTGGGTGATCTCGTGCAATGAGTGTCCATGTGGATCAAGCAG	4800
O	4801	agtgagtggaaggaagaaaggtgtccctccctgggctcagggaaatcctaagctcgaagttc	4860
D	4801	AGTGAGTGAGGAGGAGGAGAGGTGCTTCCCTGGCTTAGGAAATCATAACTGGAAGTTC	4860
O	4861	ccaccctgctcaaccctgctgtctgtctgtcgcagccctgcatgtggcgcgcttaagacca	4920
D	4861	CCACCTCTCCATCCCTTCCCTGCTGTCTGTCTCCACGCTCATGGGCGCGCGCTTAAGGCCA	4920
O	4921	acttgaagagacatccccaaggtttctgatgtgcgtccctccctccgaattgaactcta	4980
D	4921	ACTTGAAGAGACATCTCCCAAGAGTCTGATGGTGCTCCCTCTCTGAGATGACTTA	4980
O	4981	tggagcagcgtgttctaactatccagccggagagaagaagcagaaactggagatggtgcgtg	5040
D	4981	TGGAGCACTGTCTTAACATATCCACCGGAGAGAAAGACTGTGACTCGGATGGCTGG	5040

[illegible]

QY	6121	agcttcctgcgcacacttgcgcgcgaataatgcagatgcctgcgcgcgaacgaatgtataccgga	6180
Db	6121	AGCTTCCTGCTGACACTTTTGCCCGCAAAATAGATCCAGTCTGTCGACACGCAATGTCACCGGA	6180
QY	6181	gctctcagtcagcccatcctgcacagtcggaggacatgaaaggaatggatcttgctctgcttc	6240
Db	6181	GGCTTCAGTCAGCCCATCTCGACAGTGGGAGACATGAGAGGAGGGATTTGGCCCTGTGCTTC	6240
QY	6241	tgctttatcagctcctcagctcacgaaggagatgtactagtcgcgtgaagttacotacagt	6300
Db	6241	TGCTTTATTAGTCTTCAGCTCAGCTCACGAGGAGGAGTGTCTATGTCCTGATAGTTCACAGT	6300
QY	6301	actggttaacttaactttatgtctcactgcgtccactttgtctgtaattggaagctctctt	6360
Db	6301	ACTGTTAAATTAATTAATTTATTTGCTCTCACTGCTCAATTTTGTGCTGAATTTGAGCGCTCTTT	6360
QY	6361	tgacctcttctcagacataagaatcggagcctctctgcataccgaactgttaagtaaatctt	6420
Db	6361	TGACCTCTTCTTCAGCATGAGAAATGGAGCGCTTCTGTGATCCGAAATGTTAAGTAAATTTT	6420
QY	6421	aatgataccatttcataatttttccacacatcgggaagaaattgtatgtgtccattcaagcag	6480
Db	6421	AATGATGTCATTTCATATTTTTCACACATCGGAGAAAGAAATTTGTATGTTGTCATTACGACG	6480
QY	6481	caggac	6486
Db	6481	CAGGAC	6486
RESULT 2			
CNS01DX2			
LOCUS	CNS01DX2	166308 bp DNA	PRI
DEFINITION	Human chromosome 14 DNA sequence BAC R-164H13 of library RPCI-11		26-APR-2001
ACCESSION	AL139020	from chromosome 14 of Homo sapiens (human), complete sequence.	
VERSION	AL139020.5	GI:13539193	
KEYWORDS	HTG.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 166308) Hellig,R., Petit,J.L., Vico,Y., Dasilva,C., Robert,C., Winkler,P., Brottier,P., Catilico,L., Barbe,V., Pelletier,E., Attignene,A.,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Craud,C., Geyrhofer,G., Saurin,W. and Weissenbach,J.		
TITLE	Sequencing of the human chromosome 14		
JOURNAL	Unpublished		
REFERENCE	Genoscope.		
AUTHORS	2 (bases 1 to 166308)		
TITLE	Direct Submission		
JOURNAL	Submitted (26-APR-2001) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		
COMMENT	On Apr 3, 2001 this sequence version replaced gi:12274871.		

```

Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: SequRel@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-1070N10
Downstream BAC (overlapping the SP6 end) : R-185P18 (AC-AL33167)
----- Summary Statistics -----
Assembly program: Phrap; version 2.0
Quality coverage: 6.03x in Q20 bases; sum-of-contigs
-----
Overall quality chart :
Range      :      bases
0          :      4
1 - 9     :

```

[illegible]

Db 23141 AAGATGAGGAGGAGAACCTGGGTGACTGTGCTGGCTTCAATCCCTGCTAGGG 23200
Qy 301 aatggagcaggcctcccaaggagcagcagagtgagctcctggcagcagagagcgtgtgg 360
Db 23201 AATGGGCGAGGGCTCTCCAGGGGAGAGTAGTCTGGGACAGAGGAGAGGCTGTGG 23260
Qy 361 gagagctgcagcactgaacccctgcctgtgtggagccggtgtgggtgtcaagagggcgct 420
Db 23261 GAGGGCTGCGCACTGACCCCTGCCCCGTGTGGACCGCGGTGGGGTCAAGAGGGCGCTT 23320
Qy 421 ctaccccgcacttgagaaactactctgtgtcaggtctagagcgagcaatgtccatgcc 480
Db 23321 CTCACCCGCACTGGAAACTCACTTCTGTGAGGCTGTAGGAGCGCAGCAATGTCCATGCC 23380
Qy 481 cagccctgagcccaagaaacaccccccgttaaaggagacacagagcaagctttccacgt 540
Db 23381 CAGCCCTGAGCCCAAGAACACCCCCCTTAAGGGACACAGGCAAGCTTATCCACATG 23440
Qy 541 agataatgtgtcctgtgtgtgtgaagcagagctaaagtgagtgagggcttagtgcatt 600
Db 23441 AGATAATGTGTGCTGTGCTGTGTAAGCCGAGCTAAGGTACCTAGGCGTGTAGTGCATT 23500
Qy 601 cccagtgccctgtcgtggagagcccaaatgggagcagctattagagctgggcttggagat 660
Db 23501 CCCAGTGCCTGCTGGGAGGCGCCCAAAATGGGGAGCTATTGAGCTGGCTTGTGGGAT 23560
Qy 661 gagttagagatctccaggtctagaagagagcagagtagtataagcaaaagcattgag 720
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (Baes 1 to 210791)		
	Healing,R., Pettit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brothier,P., Catcollco,L., Barde,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., debernardinis,V., Crnaud,C., Gyapay,G., Saurin,W. and Weissensbach,J.		
TITLE	Sequencing of the human chromosome 14		

TITLE

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 HTG: ACTIVEFTN.
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 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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 Helling, R., Pett, J.L., Vico, V., Dasilva, C., Robert, C., Winkler, P.,
 Brothier, P., Cattolico, L., Barbe, V., Pelleitier, E., Arnaud, C.,
 Levy, M., Eckmeier, R., Bruls, T., debernardinis, V., Criau, C.,
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 Sequencing of the human chromosome 14

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ORIGIN

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Matches 1656; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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REFERENCE	1 (bases 1 to 3144)		
AUTHORS	Saitou,M., Sugimoto,J., Hatakeyama,T., Russo,G. and Isobe,M.		
TITLE	Identification of the TCOL6 genes within the breakpoint cluster		
JOURNAL	region on chromosome 14q32 in T-cell leukemia		
MEDLINE	Oncogene 19 (23), 2796-2802 (2000)		
REFERENCE	20309940		
AUTHORS	2 (bases 1 to 3144)		
TITLE	Isobe,M., Saitou,M. and Sugimoto,J.		
JOURNAL	Direct Submission		
	Submitted (29-NOV-1999) to the DDBJ/EMBL/GenBank databases.		
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	Fax:+81-76-445-6874)		
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